SUPPLEMENTAL MATERIAL

The morphogenic protein CopD controls the spatio-temporal dynamics of PBP1a and PBP2b in *Streptococcus pneumoniae*

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Figure S1: Effect of tetracycline and/or *ezrA*-depletion on cell growth and viability. (A) WT cells were grown in C+Y medium at 37°C in the presence of increasing concentration of tetracycline. The OD₅₅₀ was read automatically every 10 min. (**B**) Western immunoblot of whole-cell lysates from $\Delta ezrA$ - P_{comX} -ezrA cells, grown to exponential phase in the presence (0.5, 1 or 2 μ M) of the ComS inducer, were probed with specific anti-EzrA (α EzrA) antibody. To estimate the relative quantity of proteins in crude extract and to compare the different lanes, we used enolase (Spr1036) as an internal standard. The enolase was detected using specific antibodies (α Enolase) and is presented in the lower part of the Figure. EzrA is indicated with a black arrow. (**C**) $\Delta ezrA$ - P_{comX} -ezrA cells were grown in C+Y medium at 37°C in the absence or presence of decreasing concentration of ComS from 2 to 0 μ M. The OD₅₅₀ was read automatically every 10 min. (**D**) Growth curves of WT and $\Delta ezrA$ - P_{comX} -ezrA strains (+ 1 μ M ComS) in presence of 1.5 ng/ml or 15 ng/ml of tetracycline. (**E**) Relative cell viability of $\Delta ezrA$ - P_{comX} -ezrA (+ 1 μ M ComS) compared to WT cells in the presence of 1.5 ng/ml or 15 ng/ml of tetracycline. Bar chart represents the mean \pm SEM.



Figure S2: Expression and functionality of the CopD-sfGFP fusion. (A) The Western immunoblot was probed with specific anti-GFP antibodies (α GFP) to determine *copD* expression in *copD-sfGfp* cells. To estimate the relative quantity of proteins in crude extract and to compare the different lanes, we used enolase (Spr1036) as an internal standard. The enolase was detected using specific antibodies (α Enolase) and is presented in the lower part of the Figure. (**B**) Growth of WT and *copD-sfGfp* strains. Strains were grown in C+Y medium at 37°C in a spectrophotometer. The OD₅₅₀ was read automatically every 10 min. Representative phase contrast microscopy images of WT and *copD-sfGfp* cells are shown below the growth curves. Scale bar, 2 μ m. (**C**) Corresponding violin plot show the distribution of the cell width as determined using MicrobeJ (56). The distribution of the cell width is shown in red for the WT strain and in green for the *copD-sfGfp* strain. The box indicates the 25th to the 75th percentile, and the whiskers indicate the minimum and the maximum values. The mean and the median are indicated with a dot and a line in the box, respectively. Statistical comparison was done using t-test. n=3 indicates the number of independent experiments with a total of 8000 cells analyzed.



Figure S3: Purification of CopDed, PBP1A_{TP} **and PBP2b**_{TP}. Proteins were overproduced in *E. coli* BL21 as 6his-tagged fusion proteins. After purification using a Ni-NTA resin, purified proteins were analyzed by SDS-PAGE.



Figure S4: Validation of the *mkate2-PBP2b* fusion. (A) Growth curves of WT and *mkate2-PBP2b* cells in C+Y medium at 37°C. The OD₅₅₀ was read automatically every 10 min. (B) Violin plot showing the distribution of the cell length (left panel) and cell width (right panel) for WT (red) and *mkate2-PBP2b* (grey) strains as determined using MicrobeJ (56). The box indicates the 25th to the 75th percentile, and the whiskers indicate the minimum and the maximum values. The mean and the median are indicated with a dot and a line in the box, respectively. Statistical comparison was done using t-test. n=3 indicates the number of independent experiments with a total of 10 000 cells analyzed. (C) Expression of *mkate2-PBP2b* mkate2-PBP2b represents the only source of PBP2b from its endogenous chromosomal locus. After SDS-PAGE and electro-blotting, the membrane was probed with anti-PBP2b antibody. As control, WT cells were also analyzed. (D) Overlays between phase-contrast and mKate2 images of *mkate2-PBP2b* cells. Scale bar, 2 μ m.



Figure S5: Validation of the *mkate2-PBP1a* **fusion.** (**A**) Growth curves of WT and P_{Zn} -*mkate2-PBP1a* cells in C+Y medium at 37°C. The OD₅₅₀ was read automatically every 10 min. (**B**) Violin plot showing the distribution of the cell length (left panel) and cell width (right panel) for WT (red) and *mkate2-PBP1a* (grey) strains as determined using MicrobeJ (56). The box indicates the 25th to the 75th percentile, and the whiskers indicate the minimum and the maximum values. The mean and the median are indicated with a dot and a line in the box, respectively. Statistical comparison was done using t-test. n=3 indicates the number of independent experiments with a total of 10 000 cells analyzed. (**C**) Expression of *mkate2-PBP1a*. The merodiploid strain P_{Zn} -*mkate2-PBP1a* expresses the chromosomal *PBP1a* and the ectopic *mkate2-PBP1a* fusion under the control of the zinc-inducible P_{zn} promoter. The two forms are indicated by arrows. After SDS-PAGE and electro-blotting, the membrane was probed with anti-PBP1a antibody. As control, WT cells were also analyzed. (**D**) Overlays between phase-contrast and mkate2 images of P_{Zn} -*mkate2-PBP1a* cells. Scale bar, 2 µm.

Table S1 - Strains and plasmids used in this study

Strain	Genotype and description	Reference	Primers (Table S2)
S. pneumoniae			
R800	S. pneumoniae R6 derivative	Gift from J P.Claverys, Toulouse, France	
Wild type	R800 rpsL1	Gift from J P.Claverys, Toulouse, France	
copD ::Janus	R800 rpsL1, copD::kan-rpsL; Kan ^R	This study	1, 2, 3, 4, 5, 6
ΔcopD	R800 rpsL1, Δ copD; Str ^R	This study	1, 2, 7, 8
copD-∆PepSY	R800 rpsL1, copD-ΔPepSY(A57-L162) ; Str ^R	This study	1, 2, 9, 10
copD-sfGfp	R800 rpsL1, copD-sfGfp; Str ^R	This study	1, 2, 10, 11, 12, 13
P _{comx} -copD	R800 rpsL1, ΔIS1167::P1::P _{comR} -comR, cpsN-O::P _{comX} -copD; Str ^R	This study	14, 15, 16, 17, 18, 19
copD ::Janus- P _{comX} -copD	R800 rpsL1, ΔIS1167::P1::P _{comR} -comR, cpsN-O::P _{comx} -copD, copD::kan-rpsI; Kan ^R	This study	1, 2
∆copD-P _{comX} - copD,	R800 rpsL1, ΔIS1167::P1::P _{comR} -comR, cpsN-O::P _{comx} -copD, ΔcopD; Str ^R	This study	1, 2
P _{comx} -sfGfp	R800 rpsL1, ΔIS1167::P1::P _{comR} -comR, cpsN-O::P _{comX} -sfGfp; Str ^R	This study	14, 15, 16, 17, 20, 21
gfp-PBP2b	R800 rpsL1, gfp-PBP2b; Str ^R	This study	22, 23, 24, 25, 26
copD::Janus- gfp-PBP2b	R800 rpsL1, gfp-PBP2b, copD::kan-rpsl; Kan ^R	This study	1, 2
∆copD-gfp- PBP2b	R800 rpsL1, gfp-PBP2b, ΔcopD; Str ^R	This study	1, 2
P _{zn} -gfp-PBP1a	R800 rpsL1, bgaA::P _{Zn} -gfp-PBP1a; Str ^R Tet ^R	Gift from C. Morlot	
copD ::Janus- P _{zn} -gfp-PBP1a	R800 rpsL1, bgaA::P _{zn} -gfp-PBP1a, copD::kan-rpsl; Kan ^R Tet ^R	This study	1, 2
∆copD-P _{Zn} -gfp- PBP1a	R800 rpsL1, bgaA::P _{Zn} -gfp-PBP1a, ∆copD; Str ^R Tet ^R	This study	1, 2
copD::Janus- gfp-PBP2b	R800 rpsL1, gfp-PBP2b, copD ::kan-rpsl; Kan ^R	This study	1, 2
gfp-ftsA	R800 rpsL1, gfp-ftsA; Str ^R	1	
copD-sfGfp- gfp-PBP2b	R800 rpsL1, gfp-PBP2b, copD-sfGfp; Str ^R	This study	1, 2
P _{zn} -mkate2- PBP1a	R800 rpsL1, P _{zn} -mkate2-PBP1a, Str ^R Tet ^R	Gift from C. Morlot	
copD::Janus- P _{Zn} -mkate2- PBP1a	R800 rpsL1, P _{zn} -mkate2-PBP1a, copD::kan-rpsl, Kan ^R Tet ^R	This study	1, 2
copD-sfgfp- P _{Zn} -mkate2- PBP1a	R800 rpsL1, P _{zn} -mkate2-PBP1a, copD- sfgfp, Str ^R Tet ^R	This study	1, 2

mkate2-PBP2b	R800 rpsL1, mkate2-PBP2b, Str ^R	This study	22, 23, 25, 27, 28
copD::Janus-	R800 rpsL1, mkate2-PBP2b, copD::kan-	This study	1, 2
mkate2-PBP2b	rpsl, Kan ^r		
copD-sfGfp-	R800 rpsL1, mkate2-PBP2b, copD-sfGfp,	This study	1, 2
mkate2-PBP2b	Str ^R		
P _{comx} -ezrA	R800 rpsL1, Δ IS1167::P1::P _{comR} -comR,	This study	14, 15, 16, 17, 29,
	cpsN-O::P _{comx} -ezrA, Str ^R		30
ezrA-Janus	R800 rpsL1, ezrA-kan-rpsL; Kan ^ĸ	This study	3, 4, 31, 32, 33, 34
ezrA-Janus-	R800 rpsL1, Δ IS1167::P1::P _{comR} -comR,	This study	31, 32
P _{comx} -ezrA	cpsN-O::P _{comX} -ezrA, ezrA-kan-rpsI ; Kan ^R		
$\Delta ezrA-P_{comX}$ -	R800 rpsL1, Δ IS1167::P1::P _{comR} -comR,	This study	31, 32, 35, 36
ezrA	$cpsN-O::P_{comx}$ -ezrA, $\Delta ezrA$; Str^{R}		
E. coli strains			
XL1-Blue	supE44 hsdR17 recA1 endA1 gyrA46 thi	2	
	$relA1 lac-F'[proAB + laclqlacZ\DeltaM15 Tn10]$		
	(<i>TCⁿ</i>)]		
BIH101	F-, cya-99, araD139, galE15, galK16,	Euromedex	
DI 24 (DE2)	rpsL1 (Str ¹), hsdR2, mcrA1, mcrB1		
BL21 (DE3)	F-, $omp I$ gai acm ion $nsas_B (r_B-m_B-) \Lambda (DE3)$	3	
DI 21 ator	[10c11ac0V5-17] gene 1 ma1 sam7 mm5]	la vitra ao a	
BLZI SLOI	F ompt gal acm ion $isas_B(r_B m_B) \land (DE3)$	Invitrogen	
(DE3)	$[nalP^+1] (\lambda^{S})$		
Plasmids			
nETPhos-conD	nETPhas derivative encoding ConD from	This study	37.38
(extra)	Met 38 to Leu 162. Amp^{R}	This study	57, 50
pETPhos-	pETPhos derivative, encodina PBP2b.	This study	39.40
PBP2b (extra)	from Met39 to Asn685, Amp ^R		
pETPhos-	pETPhos derivative, encoding PBP1a,	This study	41, 42
PBP1a (extra)	from Ser37 to Pro719, Amp ^R		
pKT25	P _{lac} -T25- kan pACYC ori	4	
pUT18C	P _{lac} -T18-, bla	4	
pKT25-zip	Plac-T25-leucine zipper region from vegst	4	
PP	GCN4. kan pACYC ori		
pUT18C-zip	<i>P_{lac}-T18-leucine zipper region from yeast</i>	4	
	GCN4. bla		
PUT18C-pbp2b	P _{lac} -T18-PBP2b bla pUC ori	5	
PUT18C-pbp2x	P _{lac} -T18-PBP2x bla pUC ori	This study	43, 44
PUT18C-	P _{lac} -T18-PBP2b(Met1-Tyr38)-	This study	45, 46, 48, 49
PBP2x/PBP2bT	PBP2x(Thr52-Asp750) bla pUC ori		
M-CD			
PUT18C-	P _{lac} -T18-PBP2x(Met1-Gly51)-	This study	47, 48, 49, 50
PBP2b/PBP2xT	PBP2b(Met39-Asn685) bla pUC ori		
M-CD			
PUT18C-pbp1a	P _{lac} -T18-PBP1a bla pUC ori	6	
PUT18C-pbp2a	P _{lac} -T18-PBP2a bla pUC ori	6	
PUT18C-	P _{lac} -T18-PBP1a(Met1-Ser37)-	This study	51, 52, 53, 54
PBP2a/PBP1aT	PBP2a(Ser79-Arg731) bla pUC ori		
M-CD			

PUT18C- PBP1a/PBP2aT M-CD	P _{lac} -T18-PBP2a(Met1-Lys78)- PBP1a(Lys38-Pro719) bla pUC ori	This study	48, 55, 56, 57
pKT25-copD	P _{lac} -T25-copD kan pACYC ori	This study	57, 58, 59, 60

References

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Number	Name	Sequence 5'-3'
1	Upstream of <i>copD</i> (-635) (+)	CACTGTACCAGGGATAGAGAAG
2	Downstream of copD (+1134) (-)	CACCATTGATGACCACTGTTTGC
3	Janus cassette (+)	CCGTTTGATTTTTAATGGATAATG
4	Janus cassette (-)	AGAGACCTGGGCCCCTTTCC
5	Janus / Upstream of <i>copD</i> (-1) (-)	CATTATCCATTAAAAATCAAACGGCCCT
		AGACCATACTGCCACAG
6	Janus / Downstream of <i>copD</i> (+488) (+)	GGAAAGGGGCCCAGGTCTCTGGTCAAT
		AAGGAGGGCCTATG
7	Upstream of <i>copD</i> (-1) (-)	CCCTAGACCATACTGCCACAG
8	Downstream of copD (+411) (+)	CTGTGGCAGTATGGTCTAGGGGGTCAA
		TAAGGAGGGCCTATG
9	copD-ΔPepSY (+)	AACTATCCAACCGTGTT
10	copD-ΔPepSY (-)	ACACGGTTGGATAGTTTCAATACTGCTG
		AGCT
11	Linker / <i>copD</i> (+429) (-)	CTGCAGGAACTCGATGTCTAGTTTTAGG
		CCCTCCTTATTGACC

Table S2 - List of primers

12	sfGfp (-)	TTATTTGTAGAGCTCATCCATGCCG
13	copD / sfGfp (+)	CGGCATGGATGAGCTCTACAAATAAGG
		TCAATAAGGAGGGCCTATG
14	<i>cpsN</i> (+308) (+)	CATCGGAACCTATACTCTTTTAG
15	<i>cpsO</i> (+800) (-)	ATAACAAATCCAGTAGCTTTGG
16	P _{comX} (0) (+)	TGAACCTCCAATAATAAATATAAAT
17	<i>cpsN/0</i> (+1106) (+)	TTTCTAATATGTAACTCTTCCCAAT
18	cpsN / copD (-)	ATTGGGAAGAGTTACATATTAGAAATCA
		TAGGCCCTCCTTATTGAC
19	$P_{comX}/copD(+)$	ATTTATATTTATTATTGGAGGTTCAATGA
		ΑΑΑΑΑΑGACAAAACAAAGCAAAAAATA
		ATC
20	P _{comx} / sfGfp (+)	TATTTATTATTGGAGGTTCAATGTCTAAA
		GGTGAAGAGTT
21	cpsN / sfGfp (-)	GAAGAGTTACATATTAGAAATTATTTGT
		ACAATTCATCCA
22	Upstream of <i>PBP2b</i> (-658) (+)	GCCGTCTTGGTCTGTCAAAGCTTC
23	Downstream of <i>PBP2b</i> (+2725) (-)	CACTATACAAAAAGAGGCCGATAGG
24	<i>gfp</i> / linker (-)	TCCGGATCCCTCGAGTTTATACAATTCAT
		CCATACCATGTG
25	Linker / PBP2b (+)	CTCGAGGGATCCGGAATGAGACTGATT
		TGTATGA
26	Upstream of PBP2b / gfp (+)	AGATTTTAAGTTAGAAATGATTTCTAAA
		GGTG
27	<i>rfp</i> / linker (-)	TCCGGATCCCTCGAGCAATTTACTAGGC
		AAAT
28	Upstream of PBP2b / rfp (+)	AGATTTTAAGTTAGAAATGAAACATCTT
		ACCG
29	P _{comx} / ezrA (+)	ATTTATATTTATTATTGGAGGTTCAATGT
		CTAATGGACAACTAATTTATTTAATGG
30	cpsN / ezrA (-)	ATTGGGAAGAGTTACATATTAGAAATTA
		AAAACGAATCGTTTCACGTGTTTTC
31	Upstream of <i>ezrA</i> (-587) (+)	CAGCCATGGGAACAGGATTTG
32	Downstream of ezrA (+2338) (-)	TTTATGATATTTAGCTGTACGAGAGTC
33	Upstream of Janus / ezrA (-)	CATTATCCATTAAAAATCAAACGGTTAA
		AAACGAATCGTTTCACGTGTTTTC
34	Dowtream of <i>ezrA</i> / Janus (+)	GGAAAGGGGCCCAGGTCTCTTAAAAGA
		AAAAGATTTTATTGTGTGAGG
35	Downstream of <i>erzA</i> (+)	CGATTGTTTCAAGTAAAAAAGGAGTTTG
		ATTAAAAGAAAAAGATTTTATTGTGTGA
	· · · · · ·	GGAGC
36	Upstream of ezrA (-)	GCTCCTCACACAATAAAATCTTTTTCTTT
		TCG
37	Extracellular domain of <i>copD</i> with BamHI	IAIGGATCCTCATAGGCCCTCCTTATTGA
	extension (-)	
38	Extracellular domain of <i>copD</i> with Ndel	
	extension (+)	AAAG
39	PBP2b with BamHI extension (-)	IAIGGAICCCTAATTCATTGGATGGTAT
		TITIGATACAG

40	PBP2b with Ndel extension (+)	GGGAATTCCATATGCAGGTTTTGAACAA
		GGATTTTTACG
41	PBP1a with BamH1 extension (-)	TATGGATCCTTATGGTTGTGCTGGTTGA
		G
42	PBP1a with Ndel extension (+)	GGGAATTCCATATGAGCAAGGCTCCTA
		GCCTATCCG
43	PBP2x with Acc65I extension (-)	TATGGTACCCGTTAGTCTCCTAAAGTTA
		ATGTAATTTTTTAATG
44	PBP2x with Xbal extension (+)	TATTCTAGAGATGAAGTGGACAAAAAG
		AGTAATC
45	PBP2b (M1-Y38) fused to PBP2x (T52-D750) (+)	TTGGTCGTTTGTTGTATACTCGCTTTGGA
		ACAGA
46	PBP2b (M1-Y38) fused to PBP2x (T52-D750) (-)	TCTGTTCCAAAGCGAGTATACAACAAAC
		GACCAA
47	pKNT25/pUT18/pUT18C-GIBSON-Xbal (-)	CTCTAGAGTCGACCTGCAG
48	pKNT25/pUT18 (+)	GTATGTTGTGTGGAATTGTGAGCGG
49	<i>PBP2x</i> (M1-M51) fused to <i>PBP2b</i> (M39-N685)	TCATTATTGGGACAGGCATGCAGGTTTT
	(+)	GAACAA
50	PBP2x (M1-M51) fused to PBP2b (M39-N685) (-	TTGTTCAAAACCTGCATGCCTGTCCCAAT
)	AATGA
51	<i>PBP1a</i> (M1-S37) fused to <i>PBP2a</i> (S79-R731) (+)	TTTTCTACTACGTTAGCTCGACCAATGTC
		AATGA
52	<i>PBP1a</i> (M1-S37) fused to <i>PBP2a</i> (S79-R731) (-)	TCATTGACATTGGTCGAGCTAACGTAGT
		AGAAAA
53	pUT18C (-)	TCGGGGCTGGCTTAACTA
54	pkNT25/pUT18C/pUT18 (+)	GTACCGAGCTCGAATTCA
55	PBP2a (M1-L78) fused to PBP1a (S38-P719) (+)	TGTTTGCTGTAGCCAAGAAGGCTCCTAG
		ССТАТС
56	<i>PBP2a</i> (M1-L78) fused to <i>PBP1a</i> (L38-P719) (-)	GATAGGCTAGGAGCCTTCTTGGCTACAG
		CAAACA
57	pKT25-GIBSON-Xbal (-)	CTCTAGAGTCGACCCTGCAG
58	pKT25-GIBSON-Acc65I (+)	CGGGTACCTAAGTAACTAAGAATTC
59	copD with Xbal extension (-)	AGGGTCGACTCTAGAGGTGAAAAAAAG
		ACAAA
60		
60	copD with Acc65I extension (-)	TATGGTACCCGTAGGCCCTCCTTATTGA